proteins based on a physical property; and

iv) a mass spectroscopy apparatus; and

b) treating said cell lysate with said separating apparatus to produce a separated protein sample; wherein said separated protein sample is collected from said separating apparatus in a plurality of fractions, each of said fractions defined by a physical property;

c) analyzing said plurality of fractions from said separated protein sample with said mass spectroscopy apparatus to produce a second protein profile map, wherein said second protein profile maps displays each protein as a separate band corresponding to said mass of said first protein sample and said second protein sample, and wherein the intensity of said band corresponds to said protein abundance of said first protein sample and said second protein sample; and

A4

d) comparing said first protein profile map and said second protein profile map.

A5

26. (Once Amended) The method of Claim 23, wherein said bands are bands of different colors.

Please renumber the Claims pages from pages "43-48" to --46-51--.

IN THE ABSTRACT:

Please renumber the Abstract page from page "49" to --52--.

REMARKS

Claims 1-34 are pending in the present case and stand rejected by the Examiner. Claims 7 and 25 have been cancelled. As such, Claims 1-6, 8-24, and 26-34 are currently pending in the present case. The Examiner has noted that the required timing for correction of drawings has changed (Office Action, pg. 2). Applicants herewith submit the required drawing corrections in the form of substitute drawings. The Examiner has also stated that the present application fails to comply with the requirements for sequence disclosures (Office Action, pg 2). The applicants

herewith submit a sequence listing. The Examiner has objected to the disclosure "because it contains an embedded hyperlinks [sic] and/or other forms of browser-executable code..." Office action, pg. 5. As requested by the examiner, the Applicants have deleted the embedded hyperlink.

Applicants note that all amendments of Claims presented herein are made without acquiescing to any of the Examiner's arguments or rejections, and solely for the purpose of expediting the patent application process in a manner consistent with the PTO's Patent Business Goals (PBG),[1] and without waiving the right to prosecute the amended Claims (or similar Claims) in the future.

I. Claim Objections

The Examiner has objected to Claims 15 and 16 as being improperly dependent (Office Action, pg. 4). The Applicants have amended Claim 15 to depend on Claim 14.

The Examiner has further objected to claims 21 and 34 "due to the misspelling "oa" as set for the therein." (Office Action, pg. 4). Applicants respectfully disagree and submit that "oa" is not a misspelling. The term "oa" is used throughout the specification (*See e.g.*, Example 2, page 33, line 7 - page 33, line 20). As such, Applicants respectfully request that the objection be withdrawn.

II. Claim Rejection

In the Office Action dated 07/26/02, the Examiner rejected Claims 1-6, 9, 11, 14, 17-24, 27, 28, 31, and 34 under 35 U.S.C. § 102 (b) as allegedly being anticipated by Chong et al. (Rapid Commun. Mass Spectrometr 12:1986 [1998]); hereinafter Chong (Office Action, pg. 3). The Applicants respectfully disagree.

In regards to Claim 28 (and dependent Claims 31 and 34), the Applicants respectfully submit that Chong does not anticipate Claim 28 because Chong does not teach all of the elements of Claim 28. In particular, Chong does not teach the claim element of "an automated sample handling apparatus configured to receive separated proteins from said reverse phase HPLC separating apparatus" or the claim element of "a mass spectroscopy apparatus configured to

[1] 65 Fed. Reg. 54603 (Sept. 8, 2000).

receive proteins from said automated sample handling apparatus." The Examiner has pointed to no teaching is Chong that describes these claim elements. As such, the Applicants respectfully request that the rejection of Claims 28, 31, and 34 be withdrawn.

In regards to Claims 1-6, 9, 11, 14, 17-24 and 27, the Applicants respectfully disagree with the rejection and submit that Claims 1-6, 9, 11, 14, 17-24 and 27 are not anticipated by Chong. However, in order to further the business interests of the Applicants and while reserving the right to prosecute the original (or similar) claims in the future, the Applicants have amended Claims 1 and 23. The amended Claims 1 and 23 require that the protein profile maps display each protein as a separate band corresponding to the mass of the protein samples, wherein the intensity of the bands corresponds to the abundance of the protein. The Examiner has pointed to not teaching in Chong that describes this claim element. As Chong does not teach this element of the claims, the Applicants respectfully submit that Chong does not anticipate Claims 1-6, 9, 11, 14, 17-24 and 27. As such, the Applicants respectfully request that the rejection be withdrawn.

The Examiner has not raised any grounds of rejection or objection for Claims 7, 8, 10, 12, 13, 25, 26, 29-0, 32, and 33. As these claims are dependent on claims that the Applicants submit are allowable, the Applicants respectfully request that these claims be allowed.

CONCLUSION

All grounds of rejection and objection of the Office Action of July 26, 2002 having been addressed, reconsideration of the application is respectfully requested. It is respectfully submitted that the Claims should be allowed. Should the Examiner have any questions, or if a telephone conference would aid in the prosecution of the present application, Applicant encourages the Examiner to call the undersigned collect at 608-218-6900.

Dated: January 24, 2003

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Appendix I
Version with markings to show changes made

In the specification:

Please amend the paragraph beginning on page 34, line 16 as follows:

The MS-Fit sequence database located in the Protein Prospector program was used for protein identification by entering the peptide masses generated by tryptic digestion. The program is available on the Internet at [http://prospector.ucsf edu] the Internet World Wide Web site of the Protein Prospector at the University of California-San Francisco. Subsequently, other relevant parameters such as protein species, molecular weight and pl range are also entered in order to narrow down the search. In the illustrative examples of the present invention, Homo sapiens was chosen as the species. Since these proteins were obtained from HPLC, no isoelectric point (pI) information was available. Thus, the pI range was set between 3 and 10. The range of molecular weight values for each search was determined by MALDI-TOF or ESI-TOF analysis. The tolerance for the search of peptides against the database was set at 2 Da for MALDI-MS spectra and 0.5 Da for QIT-reTOF-MS spectra.

In the claims:

1. A method, comprising:

a) providing:

i) a first sample comprising a plurality of proteins;

ii) a second sample comprising a plurality of proteins;

iii) a separating apparatus, wherein said separating apparatus separates proteins based on a physical property;

iv) a mass spectroscopy apparatus; and

b) treating said first and second samples with said separating apparatus to produce a first separated protein sample and a second separated protein sample, wherein said first and second separated protein samples are collected from said separating apparatus in a plurality of fractions, each of said fractions defined by a physical property;

and

c) analyzing said plurality of fractions from each of said first and second separated protein samples with said mass spectroscopy apparatus to produce a protein profile map for each of said first and second samples, wherein said protein profile maps display protein abundance and mass of said first protein sample and said second protein sample, and wherein said protein profile maps displays each protein as a separate band corresponding to said mass of said first protein sample and said second protein sample, and wherein the intensity of said band corresponds to said protein abundance of said first protein sample and said second protein sample.

8. The method of Claim [7]1, wherein said [protein abundance is expressed as] bands are bands of different colors.

15. The method of Claim [16]14, wherein said buffer comprises a compound of the formula n-octyl C_6-C_{12} glycopyranoside.

23. A method, comprising:

a) providing:

i) a cell lysate derived from a cell of unknown type, said cell lysate comprising a plurality of proteins;

ii) a first protein profile map generated by the method of Claim 1;

iii) a separating apparatus, wherein said separating apparatus separates proteins based on a physical property; and

iv) a mass spectroscopy apparatus; and

b) treating said cell lysate with said separating apparatus to produce a separated protein sample; wherein said separated protein sample is collected from said separating apparatus in a plurality of fractions, each of said fractions defined by a physical property;

c) analyzing said plurality of fractions from said separated protein sample with said mass spectroscopy apparatus to produce a second protein profile map, wherein said second protein profile maps displays each protein as a separate band corresponding

to said mass of said first protein sample and said second protein sample, and wherein the intensity of said band corresponds to said protein abundance of said first protein sample and said second protein sample; and

d) comparing said first protein profile map and said second protein profile map.

26. The method of Claim [24]23, wherein said [protein abundance is expressed as] bands are bands of different colors.